

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10 657, 404

Source: Oipe

Date Processed by STIC: 9-22-03

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- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (http://www.uspto.gov/ebc/efs/downloads/documents.htm, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

Raw Sequence Listing Error Summary

Wrapped Nucleics Wrapped Nucleics Wrapped Nucleics Wrapped Aminos Wrapped Wrapped Aminos Wrapped Wrapped Wrapped Wrapped Wrapped Wrapped Wrapped Wrapped Wrapped Wrapped Wrapped Wrapped Wrapped Wrapped Wrapped Wrapped Wrapped Wrapped Wr		
Wrapped Nucleics Wrapped Aminos Wrapped Wrapped Aminos Wrapped Wrapped Aminos Wrapped Aminos Wrapped Wrapped Wrapped Aminos Wrapped Wrapped Aminos Wrapped Wrapped Aminos Wrapped Wrapped Wrapped Aminos Wrapped Wra	CRROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 10/657, 404
Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping." 2	ATTN: NEW RULES CASES:	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
Misaligned Amino Numbering Misaligned Amino Numbering Misaligned Amino Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead. The submitted file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please casure your subsequent submission is saved in ASCII text. Sequence(s) Sequence(s) The submitted file was not saved in ASCII text. Sequence(s) Sequence(s) Sequence(s) Normally, Patenth would automatically generate this section from the revisualty coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the missing. Normally, Patenth would automatically generate this section from the subsequent amino acid sequence. Please manually copy the relevant <220>-<223> section for Artificial or Unknown sequences. Sequence(s) Normally, Patenth would automatically generate this section from the revisualty coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. Please manually copy the relevant <220>-<223> section for Artificial or Unknown sequences. Sequence(s) Missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO.X: (insert SEQ ID NO where 'X': is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. Sequence(s) Missing. If intentional, please insert the following lines for each skipped sequence (NEW RULES) New RULES) Sequence is minentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequence. <210> sequence id number company to the sequence id number	Wrapped Nucleics Wrapped Aminos	was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
Numbering use space characters, instead. 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>~223> section that some may be missing. 6 Patentin 2.0 A "bug" in Patentin version 2.0 has caused the <220>~223> section to be missing from amino acid sequence. Please manually copy the relevant <220>~223> section to the missing from a the subsequent amino acid sequence. This applies to the mandatory <220>~223> section from the previously coded nucleic acid sequence. This applies to the mandatory <220>~223> sections for Artificial or Unknown sequences. 7 Skipped Sequences (OLD RULES) (OLD RULES) (OLD RULES) (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (I) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequence. (ADOS sequence id number on on the sequence sequence id number on one of the sequence sequence for the sequence sequence for the sequence sequence for the sequence sequence for subject of \$220>\$ certain please explain location of n or Xaa, and which residue n or Xaa represents. In \$220>\$\text{ certain please explain location of n or Xaa, and which residue n or Xaa represents. In \$220>\$\text{ certain please explain location of n or Xaa, and which residue n or Xaa represents. In \$220>\$\tex	2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
ensure your subsequent submission is saved in ASCII text. Sequence(s)		The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.
each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220><223> section that some may be missing. A "bug" in PatentIn version 2.0 has caused the <220><223> section to be missing from amino acid sequences(s)	4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
"bug" sequences(s) Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. 7 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERITICS: (OD not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. 8 Skipped Sequences (NEW RULES) — missing. If intentional, please insert the following lines for each skipped sequence. (NEW RULES) — missing. If intentional, please insert the following lines for each skipped sequence. (NEW RULES) — per 1.823 of Sequence id number 9 Use of n's or Xaa's (NEW RULES) — per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or Sequence (s) — missing the <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 10001/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	5Variable Length	each n or Xaa can only represent a single residue. Please present the maximum number of each
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. 400		sequences(s) Normally, Patentln would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
Skipped Sequences (NEW RULES) Sequence id number 400> sequence id number 9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.		(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(NEW RULES) Value of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.		Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06701/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.		<210> sequence id number <400> sequence id number
Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown of is Artificial Sequence 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) Patentln 2.0 "bug" Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.		Per 1 823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.		scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
"bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	11Use of <220>	Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
13 Misuse of n/Xaa "n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>		resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
	13 Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



OIPE

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DATE: 09/22/2003
                    RAW SEQUENCE LISTING
                                                            TIME: 13:16:07
                    PATENT APPLICATION: US/10/657,404
                    Input Set : A:\seq listing.txt
                    Output Set: N:\CRF4\09222003\J657404.raw
     3 <110> APPLICANT: University of Strathclyde
            Halbert, Gavin
     5
             Owens, Moira
             Baillie, George
     8 <120> TITLE OF INVENTION: Non-Naturally Occurring Lipoprotein Particle
    10 <130> FILE REFERENCE: P07885US-CIP
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/657,404
C--> 13 <141> CURRENT FILING DATE: 2003-09-08
     15 <150> PRIOR APPLICATION NUMBER: PCT/GB97/02610
     16 <151> PRIOR FILING DATE: 1997-09-25
     18 <150> PRIOR APPLICATION NUMBER: GB 9620153.8
                                                        Does Not Comply
                                                        Corrected Diskette Needed
     19 <151> PRIOR FILING DATE: 1996-09-27
     21 <160> NUMBER OF SEQ ID NOS: 9
     23 <170> SOFTWARE: PatentIn version 3.1
     25 <210> SEQ ID NO: 1
     26 <211> LENGTH: 11
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                                              surmary report
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     31 <221> NAME/KEY: misc feature
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     38 1
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     53 Thr Thr Arg Leu Thr Arg Lys Arg Gly Leu Lys
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     63 <221> NAME/KEY: misc_feature
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68 <221> NAME/KEY: misc feature

DATE: 09/22/2003

TIME: 13:16:07

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Input Set : A:\seq listing.txt
                     Output Set: N:\CRF4\09222003\J657404.raw
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     72 <220> FEATURE:
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     74 <223> OTHER INFORMATION: Retinoic acid linked at N-terminus of peptide analogue
     77 <400> SEQUENCE: 3
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     94 <221> NAME/KEY: misc feature
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     126 Tyr Lys Leu Gln Gly Thr Thr Arg Leu Thr Arg Lys Arg Gly Leu Lys
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     127 1
     130 Leu Ala Thr Ala Leu Ser
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     134 <210> SEQ ID NO: 6
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/657,404

DATE: 09/22/2003

TIME: 13:16:07

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218 Lys Leu Glu Gly Thr Thr Arg Leu Thr Arg Lys Arg Gly Leu Lys Leu

10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/657,404

216 <400> SEQUENCE: 9

223

222 Ala Thr Ala Leu Ser Leu Phe Leu Phe

20

VERIFICATION SUMMARY

DATE: 09/22/2003 TIME: 13:16:08

PATENT APPLICATION: US/10/657,404

Input Set : A:\seq listing.txt

Output Set: N:\CRF4\09222003\J657404.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:28 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:44 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:60 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
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L:107 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:137 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:162 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7